

## SEQUENCE LISTING

<110> APPLICANT: Ganymed Pharmaceuticals AG  
 Sahin, Ugur  
 Tureci, Oezlem  
 Koslowski, Michael

<120> TITLE OF INVENTION: Genetic Products Differentially Expressed In Tumors And The Use Thereof

<130> FILE REFERENCE: 4883-0001

<140> CURRENT APPLICATION NUMBER: US/10/537,002

<141> CURRENT FILING DATE: 2005-05-20

<150> PRIOR APPLICATION NUMBER: PCT/EP2003/013091

<151> PRIOR FILING DATE: 2003-11-21

<150> PRIOR APPLICATION NUMBER: DE 102 54 601.0

<151> PRIOR FILING DATE: 2002-11-22

<160> NUMBER OF SEQ ID NOS: 141

<170> SOFTWARE: PatentIn version 3.1

<210> SEQ ID NO 1

<211> LENGTH: 1875

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

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&lt;211&gt; LENGTH: 777

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 4

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&lt;211&gt; LENGTH: 3213

&lt;212&gt; TYPE: DNA

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&lt;213&gt; ORGANISM: Homo sapiens

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&lt;211&gt; LENGTH: 180

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Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg
35      40      45
Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val
50      55      60
Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu
65      70      75
Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr
85      90      95
Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val
100     105     110
Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
115     120     125
Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val
130     135     140
Ile Gly Ser Leu Val Ala Trp Leu Leu Gly Ile Gln Glu Gly Gly
145     150     155
Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Arg Phe Pro
165     170     175
Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Phe Cys Ser Leu
180     185     190
Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln
195     200     205
Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu
210     215     220
Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg
225     230     235
Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg
245     250     255
Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp
260     265     270
Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala
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Met Thr Ala Gly Arg Ser Gln Glu Arg Arg Ala Gln Glu Met Gly Arg
1      5      10      15
Gly Ser Val Gln Gly Leu Asp Leu Lys Gly Asp Leu Glu Phe Phe Thr
20      25      30
Ala Pro Met Leu Ser Leu Arg Ser Phe Val Phe Val Gly Val Gly Ser

```

## 4883-0001 substitute.txt

```

      35      40      45
Gly Leu Thr Ser Ser His Ile Pro Ala Gln Arg Trp Ala Glu Trp Gly
50 55 60
Gln Cys Leu Ala Pro Pro Ala Arg Ser Leu Leu Thr Ser Gly Ser Leu
65 70 75 80
Cys Cys Pro Arg Thr Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser
85 90 95
Asp Leu Thr Trp Pro Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu
100 105 110
Gly Val Leu Leu Val Leu Gly Leu Leu Asn Ser Leu Ala Leu Trp
115 120 125
Val Phe Cys Cys Arg Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met
130 135 140
Thr Asn Leu Ala Val Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe
145 150 155 160
Val Leu His Ser Leu Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu
165 170 175
Ser Gln Gly Ile Tyr Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val
180 185 190
Thr Ala Ile Ala Val Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg
195 200 205
Ala Arg Gly Leu Arg Ser Pro Arg Gln Ala Ala Val Cys Ala Val
210 215 220
Leu Trp Val Leu Val Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly
225 230 235 240
Ile Gln Glu Gly Gly Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn
245 250 255
Ser Met Ala Phe Pro Leu Leu Gly Phe Tyr Leu Pro Leu Val Val
260 265 270
Val Phe Cys Ser Leu Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro
275 280 285
Thr Asp Val Gly Gln Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val
290 295 300
Trp Ala Asn Leu Leu Val Phe Val Val Cys Phe Leu Pro Leu His Val
305 310 315 320
Gly Leu Thr Val Arg Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu
325 330 335
Glu Thr Ile Arg Arg Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala
340 345 350
Asn Cys Cys Leu Asp Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe
355 360 365
Gln Glu Ala Ser Ala Leu Ala Val Ala Pro Ser Ala Lys Ala His Lys
370 375 380
Ser Gln Asp Ser Leu Cys Val Thr Leu Ala
385 390

```

&lt;210&gt; SEQ ID NO 11

&lt;211&gt; LENGTH: 1073

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 11

```

Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
1 5 10 15
Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
20 25 30
Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
35 40 45
Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
50 55 60
Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65 70 75 80
Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
85 90 95

```

## 4883-0001 substitute.txt

Ser	Ser	Thr	Cys	Glu	Gly	Leu	Asp	Leu	Leu	Arg	Lys	Ile	Ser	Asn	Ala
Gln	Arg	Met	100	Gly	Cys	Val	Leu	Ile	Gly	Pro	Ser	Cys	Thr	Tyr	Ser
Phe	Gln	Met	115	Tyr	Leu	Asp	Thr	Glu	Leu	Ser	Tyr	Pro	Met	Ile	Ser
Gly	Ser	Phe	130	Gly	Leu	Ser	135	Cys	Asp	Tyr	Lys	Glu	Thr	Leu	Arg
Met	Ser	Pro	145	Ala	Arg	Lys	150	Leu	Met	Tyr	Phe	155	Leu	Val	Asn
Thr	Asn	Asp	165	Leu	Pro	Phe	170	Lys	Thr	Tyr	Ser	Trp	Ser	Thr	Ser
Tyr	Lys	Asn	180	Gly	Thr	Glu	185	Thr	Asp	Cys	Phe	Trp	Tyr	Leu	Asn
Leu	Glu	Ala	195	Ser	Val	Ser	200	Tyr	Phe	Ser	His	Glu	Leu	Gly	Phe
Val	Leu	Arg	210	Gln	Asp	Lys	215	Glu	Phe	Gln	Asp	Ile	Leu	Met	Asp
Arg	Lys	Ser	225	Asn	Val	Ile	230	Ile	Met	Cys	Gly	235	Gly	Pro	Glu
Lys	Leu	Lys	245	Gly	Asp	Arg	250	Ala	Val	Ala	Glu	Asp	Ile	Val	Ile
Val	Asp	Leu	260	Phe	Asn	Asp	265	Gln	Tyr	Leu	Glu	Asp	Asn	Val	Ala
Asp	Tyr	Met	275	Lys	Asn	Val	280	Leu	Val	Leu	Thr	Leu	Ser	Pro	Gly
Leu	Leu	Asn	290	Ser	Ser	Phe	295	Ser	Arg	Asn	Leu	Ser	300	Thr	Lys
Phe	Ala	Leu	305	Ala	Tyr	310	Leu	Asn	Gly	Ile	Leu	Leu	315	Phe	Gly
Lys	Ile	Phe	325	Leu	Glu	Asn	330	Gly	Ile	Thr	Thr	Pro	335	Lys	Phe
His	Ala	Phe	340	Asn	Leu	Thr	345	Glu	Gly	Tyr	Asp	Gly	350	Pro	Val
Leu	Asp	Asp	355	Trp	Gly	Asp	360	Val	Asp	Ser	Thr	Met	365	Val	Leu
Ser	Val	Asp	370	Thr	Lys	Lys	375	Tyr	Lys	Val	Leu	Leu	380	Thr	Tyr
Val	Asn	Lys	385	Thr	Tyr	Pro	390	Val	Asp	Met	Ser	Pro	395	Thr	Asp
Asn	Ser	Lys	405	Leu	Pro	Asn	410	Asp	Ile	Thr	Gly	Arg	415	Gly	Pro
Met	Ile	Ala	420	Val	Phe	Thr	425	Leu	Thr	Gly	Ala	Val	430	Val	Leu
Val	Ala	Leu	435	Leu	Met	Leu	440	Lys	Tyr	Arg	Lys	Asp	445	Tyr	Leu
Gln	Lys	Lys	450	Trp	Ser	His	455	Ile	Pro	Pro	Glu	Asn	460	Ile	Phe
Thr	Asn	Glu	465	Thr	Asn	His	470	Val	Ser	Leu	Lys	Ile	475	Asp	Asp
Arg	Asp	Thr	485	Ile	Gln	Arg	490	Leu	Arg	Gln	Cys	Lys	495	Tyr	Asp
Val	Ile	Leu	500	Lys	Asp	Leu	505	Lys	His	Asn	Asp	Gly	510	Asn	Phe
Gln	Lys	Ile	515	Glu	Leu	Asn	520	Lys	Leu	Leu	Gln	Ile	525	Tyr	Tyr
Thr	Lys	Phe	530	Tyr	Gly	Thr	535	Val	Lys	Leu	Asp	Thr	540	Met	Ile
Ile	Glu	Tyr	545	Cys	Glu	Arg	550	Gly	Ser	Leu	Arg	Glu	555	Val	Leu
Ile	Ser	Tyr	565	Pro	Asp	Gly	570	Thr	Phe	Met	Asp	Trp	575	Glu	Phe
Val	Leu	Tyr	580	Asp	Ile	Ala	585	Lys	Gly	Met	Ser	Tyr	590	Leu	His
														Ser	Ser

## 4883-0001 substitute.txt

```

      595      600      605
Thr Glu Val His Gly Arg Leu Lys Ser Thr Asn Cys Val Val Asp Ser
610 615 620
Arg Met Val Val Lys Ile Thr Asp Phe Gly Cys Asn Ser Ile Leu Pro
625 630 635
Pro Lys Lys Asp Leu Trp Thr Ala Pro Glu His Leu Arg Gln Ala Asn
645 650 655
Ile Ser Gln Lys Gly Asp Val Tyr Ser Tyr Gly Ile Ile Ala Gln Glu
660 665 670
Ile Ile Leu Arg Lys Glu Thr Phe Tyr Thr Leu Ser Cys Arg Asp Arg
675 680 685
Asn Glu Lys Ile Phe Arg Val Glu Asn Ser Asn Gly Met Lys Pro Phe
690 695 700
Arg Pro Asp Leu Phe Leu Glu Thr Ala Glu Glu Lys Glu Leu Glu Val
705 710 715 720
Tyr Leu Leu Val Lys Asn Cys Trp Glu Glu Asp Pro Glu Lys Arg Pro
725 730 735
Asp Phe Lys Lys Ile Glu Thr Thr Leu Ala Lys Ile Phe Gly Leu Phe
740 745 750
His Asp Gln Lys Asn Glu Ser Tyr Met Asp Thr Leu Ile Arg Arg Leu
755 760 765
Gln Leu Tyr Ser Arg Asn Leu Glu His Leu Val Glu Arg Thr Gln
770 775 780
Leu Tyr Lys Ala Glu Arg Asp Arg Ala Asp Arg Leu Asn Phe Met Leu
785 790 795 800
Leu Pro Arg Leu Val Val Lys Ser Leu Lys Glu Lys Gly Phe Val Glu
805 810 815
Pro Glu Leu Tyr Glu Glu Val Thr Ile Tyr Phe Ser Asp Ile Val Gly
820 825 830
Phe Thr Thr Ile Cys Lys Tyr Ser Thr Pro Met Glu Val Val Asp Met
835 840 845
Leu Asn Asp Ile Tyr Lys Ser Phe Asp His Ile Val Asp His His Asp
850 855 860
Val Tyr Lys Val Glu Thr Ile Gly Asp Ala Tyr Met Val Ala Ser Gly
865 870 875 880
Leu Pro Lys Arg Asn Gly Asn Arg His Ala Ile Asp Ile Ala Lys Met
885 890 895
Ala Leu Glu Ile Leu Ser Phe Met Gly Thr Phe Glu Leu Glu His Leu
900 905 910
Pro Gly Leu Pro Ile Trp Ile Arg Ile Gly Val His Ser Gly Pro Cys
915 920 925
Ala Ala Gly Val Val Gly Ile Lys Met Pro Arg Tyr Cys Leu Phe Gly
930 935 940
Asp Thr Val Asn Thr Ala Ser Arg Met Glu Ser Thr Gly Leu Pro Leu
945 950 955 960
Arg Ile His Val Ser Gly Ser Thr Ile Ala Ile Leu Lys Arg Thr Glu
965 970 975
Cys Gln Phe Leu Tyr Glu Val Arg Gly Glu Thr Tyr Leu Lys Gly Arg
980 985 990
Gly Asn Glu Thr Thr Tyr Trp Leu Thr Gly Met Lys Asp Gln Lys Phe
995 1000 1005
Asn Leu Pro Thr Pro Pro Thr Val Glu Asn Gln Gln Arg Leu Gln
1010 1015 1020
Ala Glu Phe Ser Asp Met Ile Ala Asn Ser Leu Gln Lys Arg Gln
1025 1030 1035
Ala Ala Gly Ile Arg Ser Gln Lys Pro Arg Arg Val Ala Ser Tyr
1040 1045 1050
Lys Lys Gly Thr Leu Glu Tyr Leu Gln Leu Asn Thr Thr Asp Lys
1055 1060 1065
Glu Ser Thr Tyr Phe
1070

```



## 4883-0001 substitute.txt

```

<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 12
Met Lys Thr Leu 5 Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
1 10 15
Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
20 25 30
Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
35 40 45
Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
50 55 60
Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65 70 75 80
Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
85 90 95
Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Pro
100 105 110

```

```

<210> SEQ ID NO 13
<211> LENGTH: 258
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 13
Met Lys Thr Leu 5 Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
1 10 15
Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
20 25 30
Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
35 40 45
Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
50 55 60
Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65 70 75 80
Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
85 90 95
Ser Ser Thr Cys Glu Gly Leu Asp Leu Arg Lys Ile Ser Asn Ala
100 105 110
Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr
115 120 125
Phe Gln Met Tyr Leu Asp Thr 135 Glu Leu Ser Tyr Pro 140 Met Ile Ser Ala
130 145
Gly Ser Phe Gly Leu Ser 150 Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu
155 160
Met Ser Pro Ala Arg 165 Lys Leu Met Tyr Phe 170 Leu Val Asn Phe Trp Lys
175
Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val
180 185 190
Tyr Lys Asn Gly Thr Glu Thr Glu Asp Cys Phe Trp Tyr 205 Leu Asn Ala
210 215
Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val
220 225
Val Leu Arg Gln Asp Lys 230 Glu Phe Gln Asp Ile 235 Leu Met Asp His Asn
240
Arg Lys Ser Asn Val 245 Thr Ser Thr Trp Arg Thr Met Ser Gln Pro Leu
250 255
Thr Ile

```

```

<210> SEQ ID NO 14
<211> LENGTH: 1070
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 14

```

## 4883-0001 substitute.txt

Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Phe Gln  
 1 5 10 15  
 Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn  
 20 25 30  
 Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala  
 35 40 45  
 Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile  
 50 55 60  
 Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala  
 65 70 75 80  
 Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg  
 85 90 95  
 Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala  
 100 105 110  
 Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr  
 115 120 125  
 Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala  
 130 135 140  
 Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu  
 145 150 155 160  
 Met Ser Pro Ala Arg Lys Leu Met Tyr Phe Leu Val Asn Phe Trp Lys  
 165 170 175  
 Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val  
 180 185 190  
 Tyr Lys Asn Gly Thr Glu Thr Glu Asp Cys Phe Trp Tyr Leu Asn Ala  
 195 200 205  
 Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val  
 210 215 220  
 Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His Asn  
 225 230 235 240  
 Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe Leu Tyr  
 245 250 255  
 Lys Leu Lys Gly Asp Arg Ala Val Ala Asp Ile Val Ile Leu  
 260 265 270  
 Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro  
 275 280 285  
 Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Asn Ser  
 290 295 300  
 Leu Leu Asn Ser Ser Phe Ser Arg Asn Leu Ser Pro Thr Lys Arg Asp  
 305 310 315 320  
 Phe Ala Leu Ala Tyr Leu Asn Gly Ile Leu Phe Gly His Met Leu  
 325 330 335  
 Lys Ile Phe Leu Glu Asn Gly Glu Asn Ile Thr Thr Pro Lys Phe Ala  
 340 345 350  
 His Ala Phe Arg Asn Leu Thr Phe Glu Gly Tyr Asp Gly Pro Val Thr  
 355 360 365  
 Leu Asp Asp Trp Gly Asp Val Asp Ser Thr Met Val Leu Leu Tyr Thr  
 370 375 380  
 Ser Val Asp Thr Lys Lys Tyr Lys Val Leu Leu Thr Tyr Asp Thr His  
 385 390 395 400  
 Val Asn Lys Thr Tyr Pro Val Asp Met Ser Pro Thr Phe Thr Trp Lys  
 405 410 415  
 Asn Ser Lys Leu Pro Asn Asp Ile Thr Gly Arg Gly Pro Gln Ile Leu  
 420 425 430  
 Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu Leu  
 435 440 445  
 Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg  
 450 455 460  
 Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu  
 465 470 475 480  
 Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg  
 485 490 495  
 Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Arg

## 4883-0001 substitute.txt

500														
Val	Ile	Leu	Lys	Asp	Leu	Lys	His	Asn	Asp	Gly	Asn	Thr	Glu	Lys
Gln	Lys	Ile	Glu	Leu	Asn	Lys	Ile	Asp	Tyr	Tyr	Asn	Leu	Thr	Lys
Tyr	Gly	Thr	Val	Lys	Leu	Asp	Thr	Met	Ile	Phe	Gly	Val	Ile	Glu
545					550					555				560
Cys	Glu	Arg	Gly	Ser	Leu	Arg	Glu	Val	Leu	Asn	Asp	Thr	Ile	Tyr
				565					570					575
Pro	Asp	Gly	Thr	Phe	Met	Asp	Trp	Glu	Phe	Lys	Ile	Ser	Val	Leu
				580					585				590	
Asp	Ile	Ala	Lys	Gly	Met	Ser	Tyr	Leu	His	Ser	Ser	Lys	Thr	Glu
		595					600					605		Val
His	Gly	Arg	Leu	Lys	Ser	Thr	Asn	Cys	Val	Val	Asp	Ser	Arg	Met
		610				615					620			Val
Val	Lys	Ile	Thr	Asp	Phe	Gly	Cys	Asn	Ser	Ile	Leu	Pro	Pro	Lys
625					630					635				640
Asp	Leu	Trp	Thr	Ala	Pro	Glu	His	Leu	Arg	Gln	Ala	Asn	Ile	Ser
				645					650					655
Lys	Gly	Asp	Val	Tyr	Ser	Tyr	Gly	Ile	Ile	Ala	Gln	Glu	Ile	Leu
				660					665				670	
Arg	Lys	Glu	Thr	Phe	Tyr	Thr	Leu	Ser	Cys	Arg	Asp	Arg	Asn	Glu
		675					680							Lys
Ile	Phe	Arg	Val	Glu	Asn	Ser	Asn	Gly	Met	Lys	Pro	Phe	Arg	Pro
		690				695					700			Asp
Leu	Phe	Leu	Glu	Thr	Ala	Glu	Glu	Lys	Glu	Leu	Val	Tyr	Leu	Leu
705					710					715				720
Val	Lys	Asn	Cys	Trp	Glu	Glu	Asp	Pro	Glu	Lys	Arg	Pro	Asp	Phe
				725						730				735
Lys	Ile	Glu	Thr	Thr	Leu	Ala	Lys	Ile	Phe	Gly	Leu	Phe	His	Gln
				740					745				750	
Lys	Asn	Glu	Ser	Tyr	Met	Asp	Thr	Leu	Ile	Arg	Arg	Leu	Gln	Leu
				755										Tyr
Ser	Arg	Asn	Leu	Glu	His	Leu	Val	Glu	Glu	Arg	Thr	Gln	Leu	Lys
		770				775					780			
Ala	Glu	Arg	Asp	Arg	Ala	Asp	Arg	Leu	Asn	Phe	Met	Leu	Leu	Pro
					790					795				Arg
Leu	Val	Val	Lys	Ser	Leu	Lys	Glu	Lys	Gly	Phe	Val	Glu	Pro	Glu
				805					810				815	Leu
Tyr	Glu	Glu	Val	Thr	Ile	Tyr	Phe	Ser	Asp	Ile	Val	Gly	Phe	Thr
				820					825				830	
Ile	Cys	Lys	Tyr	Ser	Thr	Pro	Met	Glu	Val	Val	Asp	Met	Leu	Asn
		835					840					845		Asp
Ile	Tyr	Lys	Ser	Phe	Asp	His	Ile	Val	Asp	His	His	Asp	Val	Tyr
		850				855				860				Lys
Val	Glu	Thr	Ile	Gly	Asp	Ala	Tyr	Met	Val	Ala	Ser	Gly	Leu	Pro
865					870					875				880
Arg	Asn	Gly	Asn	Arg	His	Ala	Ile	Asp	Ile	Ala	Lys	Met	Ala	

## 4883-0001 substitute.txt

```

Thr Pro  Pro Thr Val Glu Asn  Gln Gln Arg Leu Gln  Ala Glu Phe
1010                                     1015      1020
Ser Asp  Met Ile Ala Asn  Ser  Leu Gln Lys Arg Gln  Ala Ala Gly
1025                                     1030      1035
Ile Arg  Ser Gln Lys Pro Arg  Arg Val Ala Ser Tyr  Lys Lys Gly
1040                                     1045      1050
Thr Leu  Glu Tyr Leu Gln Leu  Asn Thr Thr Asp Lys  Glu Ser Thr
1055                                     1060      1065
Tyr Phe                                     Lys
1070

```

&lt;210&gt; SEQ ID NO 15

&lt;211&gt; LENGTH: 93

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 15

```

Met Lys Leu Val Thr Ile Phe Leu Leu Val Thr Ile Ser Leu Cys Ser
1      5      10      15
Tyr Ser Ala Thr Ala Lys Leu Ile Asn Lys Cys Pro Leu Pro Val Asp
20      25      30
Lys Leu Ala Pro Leu Pro Leu Asp Asn Ile Leu Pro Phe Met Asp Pro
35      40      45
Leu Lys Leu Leu Leu Lys Thr Leu Gly Ile Ser Val Glu His Leu Val
50      55      60
Glu Gly Leu Arg Lys Cys Val Asn Glu Leu Gly Pro Glu Ala Ser Glu
65      70      75      80
Ala Val Lys Lys Leu Glu Ala Leu Ser His Leu Val
85      90

```

&lt;210&gt; SEQ ID NO 16

&lt;211&gt; LENGTH: 261

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 16

```

Met Ala Val Thr Ala Cys Gln Gly Leu Gly Phe Val Val Ser Leu Ile
1      5      10      15
Gly Ile Ala Gly Ile Ile Ala Ala Thr Cys Met Asp Gln Trp Ser Thr
20      25      30
Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val Phe Asn Tyr Gln Gly
35      40      45
Leu Trp Arg Ser Cys Val Arg Glu Ser Ser Gly Phe Thr Glu Cys Arg
50      55      60
Gly Tyr Phe Thr Leu Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65      70      75      80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
85      90      95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100      105      110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115      120      125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130      135      140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145      150      155      160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165      170      175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180      185      190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195      200      205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210      215      220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile

```

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225 230 235 240  
 Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser  
 245 250 255  
 Lys His Asp Tyr Val  
 260

<210> SEQ ID NO 17  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <400> SEQUENCE: 17  
 Asp Gln Trp Ser Thr Gln Asp Leu Tyr Asn  
 1 5 10

<210> SEQ ID NO 18  
 <211> LENGTH: 11  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <400> SEQUENCE: 18  
 Asn Asn Pro Val Thr Ala Val Phe Asn Tyr Gln  
 1 5 10

<210> SEQ ID NO 19  
 <211> LENGTH: 47  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <400> SEQUENCE: 19  
 Met Ala Val Thr Ala Cys Gln Gly Leu Gly Phe Val Val Ser Leu Ile  
 1 5 10 15  
 Gly Ile Ala Gly Ile Ile Ala Ala Thr Cys Met Asp Gln Trp Ser Thr  
 20 25 30  
 Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val Phe Asn Tyr Gln  
 35 40 45

<210> SEQ ID NO 20  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 20  
 aggtacatga gcatcagcct g 21

<210> SEQ ID NO 21  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 21  
 gcagcagttg gcatctgaga g 21

<210> SEQ ID NO 22  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 22  
 gcaatagaca ttgccaagat g 21

<210> SEQ ID NO 23  
 <211> LENGTH: 21

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```

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 23
aacgctgttg attctccaca g
21

<210> SEQ ID NO 24
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 24
ggatcctcct ttagttccca ggtgagtcag aac
33

<210> SEQ ID NO 25
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 25
tgctctggag gctagcgttt c
21

<210> SEQ ID NO 26
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 26
accaatcatg ttagcctcaa g
21

<210> SEQ ID NO 27
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 27
agctatggga tcatgcaca g
21

<210> SEQ ID NO 28
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 28
cctttgagct ggagcatctt c
21

<210> SEQ ID NO 29
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 29
ctttctagct ggagacatca g
21

<210> SEQ ID NO 30
<211> LENGTH: 21

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## 4883-0001 substitute.txt

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 30
caccatggta ctgtcaacat c
21

<210> SEQ ID NO 31
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 31
atgtcataca agacagagat c
21

<210> SEQ ID NO 32
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 32
tctgccttgt acagctgtgt c
21

<210> SEQ ID NO 33
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 33
tctgtggtat tcagctgcaa g
21

<210> SEQ ID NO 34
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 34
tactcaggaa aatttcacct tg
22

<210> SEQ ID NO 35
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 35
gaccacaaca ggaaaagcaa tgtgacc
27

<210> SEQ ID NO 36
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 36
gatagaattg aacaagattg ac
22

<210> SEQ ID NO 37
<211> LENGTH: 21

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## 4883-0001 substitute.txt

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 37
cagcctttgt agttactctg c                                     21

<210> SEQ ID NO 38
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 38
tgtcacacca agtgtgatag c                                     21

<210> SEQ ID NO 39
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 39
ggttcgtggt ttactgatt gggattgc                             28

<210> SEQ ID NO 40
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 40
cggctttgta gtgttttct tctggtg                             27

<210> SEQ ID NO 41
<211> LENGTH: 3814
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 41
ctattgaagc caccctgcta ggacaatgaa attcttcagt tacattctgg tttatcgccg      60
attctctctc gtggttttca ctgtgttgggt ttactacct ctgcccacgt tcctccacac      120
caaggaaagc gaatgtgcct acacactctt tgtggtcgcc acattttggc tcacagaagc      180
attgctcttg tcggtaacag ctttgctacc tagtttaagt ttaccatagt ttgggatcat      240
gccttctaag aaggtggcat ctgcttattt caaggatttt cacttactgc taattggagt      300
tatctgttta gcaacatcca tagaaaaatg gaatttgcac aagagaattg ccttgaaaaa      360
ggtgatgatg gttggtgtaa atcctgcatg gctgacgctg ggtttcatga gcagcactgc      420
ctttttgtct atgtggctca gcaacacctc gacggctgcc atggtgatgc ccattcgcca      480
ggctgtagtg cagcagatca tcaatgcaga agcagaggtc gaggccactc agatgactta      540
cttcaacgga tcaaccaccc acggaactaga aattgatgaa agtgttaatg gatcatgaaa      600
aaatgagagg aaagagaaaa caaaaccagt tccaggatac aataatgata cagggaaaaa      660
ttcaagcaag gtggagttyg aaaagaactc aggcagataga accaaatcgc gaacaaagaa      720
ggggccacgt acacgttaac ttcgtgtttt gtgcattgcc tactcttcta ccattggtyg      780
actgacaaca atcactggta cctccaccaa ctgatcttt gcagagtatt tcaatacacg      840
ctatctgtac tgtcgttgcc tcaactttgg atcatggttt acgttttctc tcccagctgc      900
ccttatcatt ctactcttat cctggatctg gcttcagtgg cttttccctag gattcaattt      960
taaggagatg ttcaaatgtg gcaaaaccaa aacagtcctc aaaaagcctt gtgctgaggt      1020
gattaagcaa gaataccaaa agcttgggcc aataagtgat caagaattgt tgactcttgt      1080
cctctcattt ataattggctc tgcctatggt tagtcgagac cccgattgtt ttctcgtgtg      1140
gtctgcactt ttttcagagt accctggttt tgctacagat tcaactgtgt ctttacttat      1200
agggtctgcta ttctttctta tccagcttaa gacactgact aaaaactcac ctacaggaga      1260
aattgttgct ttgtattact ctccactgat tacttggaaa gaattccagt cattcatgcc      1320
ctgggatata gccattcttg ttggtggagg gtttgccctg gcagatggtt gtgaggagtc      1380
tggattatct aagtggatag gaaataaatt atctcctctg ggttcattac cagcatggct      1440

```



# 4883-0001 substitute.txt

aataattctg	atatcttctt	tgtatgtgtg	atctttaact	gaggttagcca	gcaatccagc	1500
taccattata	ctctttctcc	caatattatc	tccattggcc	gaagccattc	atgtgaacc	1560
ctctttatat	ctgatacctt	ctactctgtg	tacttcaatt	gcattccctc	taccagtagc	1620
aaatccacc	aattgctatt	ctctttcata	tggtcatctg	aaagtctctg	acatgggttaa	1680
agctggagct	gggtgcaca	tgtgtgtgtg	tgctgtgggt	atgtctggga	tatgtacttg	1740
tgctgttacc	atgtgtgacc	ctcacactta	cccttctgtg	gctctctgta	tgagttaatga	1800
gaccatgcca	taataagcag	aaaatttctg	actatcttgc	ggtaatttct	ggaagacatt	1860
aatgattgac	tgtaaaatgt	ggctctaaat	aactaatgac	acacatttaa	atcagtttatg	1920
gtgtagctgc	tgcaattccc	gtgaataccc	gaaacctgct	gggtataact	agagtccata	1980
ttgtttattg	cagtgcacct	aaagagcatt	tatgtgctct	catcaagaag	cccatgtttt	2040
gagattttgc	tcatgaacca	tctgcaactt	gcttcatcat	aagaataatt	tataacttga	2100
ccttcaaa	gattagagca	tttgtttcat	cttacagtgt	gagttcaatt	taacatttta	2160
aatgcaattt	attattttcag	aaatttccca	tgaaactaaa	aatagaaaaa	aagatataca	2220
agtttaattc	gtacttggat	aaatcatttc	tgcattgttg	ttccagagaa	tttgctgaga	2280
aatcaaac	atggctcatc	gggtgatga	agaaaaggtt	aatctaaatg	atatgtgcatt	2340
ttctctattt	aaaaaatcca	attggattat	tcttaata	tacatgtaat	atgaaaaattg	2400
agattgaagc	actaaattcca	aaattatggc	tgaatatact	aaataacaga	aaagtctacag	2460
ataagaattt	attttctact	aacctctatg	tagtgttaat	ataattctga	tttttatgat	2520
attggcacac	tgagaaattg	attttgtaga	gctatggata	aggcttgcta	gtatttgac	2580
tattatgata	gtatagttag	aaaggaagac	tgaacactat	ataattctta	acatattttt	2640
gtatatgagt	aacaaatttg	cttaagtgtt	tatcttagtt	cagaataaca	taattgtcata	2700
tgttaaaaa	aaagagatgt	agaaaactaa	atgaattatc	actgtgtata	cagacagaaa	2760
aatcacataa	ctctggtgtg	ttaacattgc	aatgaaaaaa	tgaaaaaaag	agggaaaaaa	2820
gaataagaat	gaaaaactgt	gacgtattac	aaaaacagaa	aataaattgt	ttaaaaactaa	2880
atcaaaaaga	aaaaaactgt	acattttaac	aaaaatggga	taagaattagt	ctcttagaag	2940
tgaggatgcg	taaaagaaatg	agtttccaat	taccctgatg	tgacaattac	acattgtaga	3000
caggtagacca	aatatcacat	acacccccaa	aaatatgtaca	aaatatatat	atcaataaat	3060
aaatttttta	agagtaagtg	ctattggcat	tccaaaattc	agctaaagga	aaaattgatca	3120
aaacaaaagt	aggggtcac	gttagcaaaa	gatgacagat	ttatatcaca	gcaatttctca	3180
tgctaaaaat	acacaaaaag	acaaagcaaa	aaataaacct	ttgctttttt	tttttttttt	3240
tttttttttt	gagacaggat	ctgcctctgt	cgcccaggct	ggagtgcagt	ggcgggattct	3300
cggtctcact	caagctccgc	ctcccagggt	cacgccattc	tcctgcctca	gccaaacctt	3360
tgctattttt	aattcttcgt	ggcaccttcc	agctgttact	gaccttgtca	ttttttgttc	3420
aaataagatt	atttacaac	ttattcttga	aactaaatat	agtaaagagg	gtttttaaaa	3480
taatatttta	catacgaatt	attaattggc	catgttcaatt	atttatctat	gtttattaat	3540
gggccaatgc	aaaaaatcat	tttttcaaa	aaaaatttgt	ccatgtaagg	ctttaaattat	3600
aatattgtct	ctttgtataa	ctcttctatg	tttttctatg	attattgttc	ctttccctac	3660
catattttac	acatgtattt	ataatctgta	gtattttatta	catttctgct	tttttctagt	3720
catttcaatt	atcactgctg	aaatgcata	gatcatggat	gcatttttat	tatgaaaaaa	3780
taaaatgact	tttcaaat	aaaaaaaaaa	aaaa			3814

<210> SEQ ID NO 42  
 <211> LENGTH: 734  
 <212> TYPE: DNA  
 <213> ORGANISM: Homo sapiens  
 <400> SEQUENCE: 42

caggacaatg	aaattcttca	gttacattct	ggtttatcgc	cgattttctt	tcgtggtttt	60
cactgtgttg	gttttactac	ctctgcccat	cgctctccac	accaaggaag	cagaattgtgc	120
ctcacacttc	tttgtggctg	ccacattttg	gctcacagaa	cgattgcctc	tgctgggtaac	180
agctttgtcta	cttagtttaa	gtttaccat	gtttgggatc	atgctctcta	agaaagtggc	240
atctgcttat	ttcaaggatt	ttcacttact	gctaattgga	gttatctgtt	tagcaacatc	300
catagaaaaa	tggaaatttg	acaagagaat	tgctctgaaa	atggtgtatga	tggttggtgt	360
aaatctctga	tggctgacgc	tgggggttat	gagcagcact	gcccttttgt	ctatgtggtc	420
cagcaacacc	tcgacggctg	ccatgtgtgat	gccattgctg	gaggtctgtg	tcgcagcagat	480
catcaatgca	gaagcagagg	tcgaggccac	tcagatgact	tacttcaacg	gatcaaccaa	540
ccacggacta	gaattgtatg	aaagtgttaa	tggacatgaa	ataaataaga	ggaagagaga	600
aacaaaacca	gttccaggat	acaataatga	tacagggaaa	atttcaagca	aggtggagtt	660
ggaaaagact	gtttactac	tgaatgaag	ctattctcct	gactaaacat	aactgaaaaa	720
ccattcatta	aatg					734

<210> SEQ ID NO 43  
 <211> LENGTH: 539  
 <212> TYPE: DNA

## 4883-0001 substitute.txt

<213> ORGANISM: Homo sapiens  
<400> SEQUENCE: 43

gccactcaga	tgacttactt	caacggatca	accaaaccacg	gactagaagt	tgatgaaagt	60
gttaattggac	atgaaaataaa	tgagaggaaa	gagaaaaacaa	aaccagttcc	aggatacaat	120
aatgatcacag	ggaaaaatttc	aagcaagggtg	gagttggaaa	agcactggaa	acttgcagtt	180
caagatggct	ccccattctc	ctctgtccat	tctgtatcgc	agctagctgc	tcaaggaaag	240
gagaaaagtg	aaggcatatg	tacttagaaa	ttattcttatt	actttctctg	atttaagagt	300
attcagattt	tctattttcaa	catcaaacaa	ttgcattttt	aaaaagaaat	ttatgtgttc	360
catgtcaaat	ttagtagtgt	gtggtgtgtt	ataatatttt	cttatatcta	cttaattttc	420
atagtattta	tagttatatg	tcctttattt	taacattttt	cttgtgcttt	taaagattat	480
ttaagattta	tttttaataa	atctttattt	cattttaaata	aaatatttta	tttaagtct	539

<210> SEQ ID NO 44  
<211> LENGTH: 556  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<400> SEQUENCE: 44

cacggactag	aaattgatga	aagtgttaat	ggacatgaaa	taaatgagag	gaaagagaaa	60
acaaaaaccag	ttccaggata	caataatgat	acagggaaaa	tttcaagcaa	ggtggagttg	120
gaaaagaact	caggcatgag	aaccaaatat	cgaacaaaga	agggccacgt	gacacgtaaa	180
cttactgtgt	tggtgattgc	ctactcttct	accattgggt	gactgacaac	aactcactgg	240
acctctacca	acttgatctt	tgcagagtat	ttcaatacat	tccatccaca	cagaagagga	300
gatcgtacaa	ggcatgtaca	caggaggcca	gaaatttgag	gcatactctg	gaactctgtc	360
tccacatctc	tgaacatcac	acagttttca	ctcttgttgc	cttcaatcct	gagaatgcac	420
caagtgacca	tctgttttta	tgtcaattac	taattagatc	atgtcacgtt	actaacctac	480
tacgttccaa	ttagctctta	ttgcatttgt	aataaaaatc	gcatactttc	ggactggcta	540
caaggttata	catgat					556

<210> SEQ ID NO 45  
<211> LENGTH: 595  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens  
<400> SEQUENCE: 45

Met	Lys	Phe	Phe	Ser	Tyr	Ile	Leu	Val	Tyr	Arg	Arg	Phe	Leu	Phe	Val
1			5						10				15		
Val	Phe	Thr	Val	Leu	Val	Leu	Leu	Pro	Leu	Pro	Ile	Val	Leu	His	Thr
			20					25				30			
Lys	Glu	Ala	Glu	Cys	Ala	Tyr	Thr	Leu	Phe	Val	Val	Ala	Thr	Phe	Trp
		35					40					45			
Leu	Thr	Glu	Ala	Leu	Pro	Leu	Ser	Val	Thr	Ala	Leu	Leu	Pro	Ser	Leu
	50					55					60				
Met	Leu	Pro	Met	Phe	Gly	Ile	Met	Pro	Ser	Lys	Lys	Val	Ala	Ser	Ala
65				70					75				80		
Tyr	Phe	Lys	Asp	Phe	His	Leu	Leu	Leu	Ile	Gly	Val	Ile	Cys	Leu	Ala
				85					90				95		
Thr	Ser	Ile	Glu	Lys	Trp	Asn	Leu	His	Lys	Arg	Ile	Ala	Leu	Lys	Met
			100					105					110		
Val	Met	Met	Val	Gly	Val	Asn	Pro	Ala	Trp	Leu	Thr	Leu	Gly	Phe	Met
		115					120					125			
Ser	Ser	Thr	Ala	Phe	Leu	Ser	Met	Trp	Leu	Ser	Asn	Thr	Ser	Thr	Ala
		130				135					140				
Ala	Met	Val	Met	Pro	Ile	Ala	Glu	Ala	Val	Val	Gln	Gln	Ile	Ile	Asn
145				150					155				160		
Ala	Glu	Ala	Glu	Val	Glu	Ala	Thr	Gln	Met	Thr	Tyr	Phe	Asn	Gly	Ser
			165					170					175		
Thr	Asn	His	Gly	Leu	Glu	Ile	Asp	Glu	Ser	Val	Asn	Gly	His	Glu	Ile
		180					185					190			
Asn	Glu	Arg	Lys	Glu	Lys	Thr	Lys	Pro	Val	Pro	Gly	Tyr	Asn	Asn	Asp
		195					200					205			
Thr	Gly	Lys	Ile	Ser	Ser	Lys	Val	Glu	Leu	Glu	Val	Asn	Ser	Gly	Met
	210					215					220				
Arg	Thr	Lys	Tyr	Arg	Thr	Lys	Lys	Gly	His	Val	Thr	Arg	Lys	Leu	Thr
225				230					235					240	

## 4883-0001 substitute.txt

Cys Leu Cys Ile Ala Tyr Ser Ser Thr Ile Gly Gly Leu Thr Thr Ile  
 245 250 255  
 Thr Gly Thr Ser Thr Asn Leu Ile Phe Ala Glu Tyr Phe Asn Thr Arg  
 260 265 270  
 Tyr Pro Asp Cys Arg Cys Leu Asn Phe Gly Ser Trp Phe Thr Phe Ser  
 275 280 285  
 Phe Pro Ala Ala Leu Ile Ile Leu Leu Ser Trp Ile Trp Leu Gln  
 290 295 300  
 Trp Leu Phe Leu Gly Phe Asn Phe Lys Glu Met Phe Lys Cys Gly Lys  
 305 310 315 320  
 Thr Lys Thr Val Gln Gln Lys Ala Cys Ala Glu Val Ile Lys Gln Glu  
 325 330 335  
 Tyr Gln Lys Leu Gly Pro Ile Arg Tyr Gln Glu Ile Val Thr Leu Val  
 340 345 350  
 Leu Phe Ile Ile Met Ala Leu Leu Trp Phe Ser Arg Asp Pro Gly Phe  
 355 360 365  
 Val Pro Gly Trp Ser Ala Leu Phe Ser Glu Tyr Pro Gly Phe Ala Thr  
 370 375 380  
 Asp Ser Thr Val Ala Leu Leu Ile Gly Leu Leu Phe Phe Leu Ile Pro  
 385 390 400  
 Ala Lys Thr Leu Thr Lys Thr Thr Pro Thr Gly Glu Ile Val Ala Phe  
 405 410 415  
 Asp Tyr Ser Pro Leu Ile Thr Trp Lys Glu Phe Gln Ser Phe Met Pro  
 420 425 430  
 Trp Asp Ile Ala Ile Leu Val Gly Gly Gly Phe Ala Leu Ala Asp Gly  
 435 440 445  
 Cys Glu Glu Ser Gly Leu Ser Lys Trp Ile Gly Asn Lys Leu Ser Pro  
 450 455 460  
 Leu Gly Ser Leu Pro Ala Trp Leu Ile Ile Leu Ile Ser Ser Leu Met  
 465 470 475 480  
 Val Thr Ser Leu Thr Glu Val Ala Ser Asn Pro Ala Thr Ile Thr Leu  
 485 490 495  
 Phe Leu Pro Ile Leu Ser Pro Leu Ala Glu Ala Ile His Val Asn Pro  
 500 505 510  
 Leu Tyr Ile Leu Ile Pro Ser Thr Leu Cys Thr Ser Phe Ala Phe Leu  
 515 520 525  
 Leu Pro Val Ala Asn Pro Pro Asn Ala Ile Val Phe Ser Tyr Gly His  
 530 535 540  
 Leu Lys Val Ile Asp Met Val Lys Ala Gly Leu Gly Val Asn Ile Val  
 545 550 555 560  
 Gly Val Ala Val Val Met Leu Gly Ile Cys Thr Trp Ile Val Pro Met  
 565 570 575  
 Phe Asp Leu Tyr Thr Pro Ser Trp Ala Pro Ala Met Ser Asn Glu  
 580 585 590  
 Thr Met Pro  
 595

&lt;210&gt; SEQ ID NO 46

&lt;211&gt; LENGTH: 224

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 46

Arg Thr Met Lys Phe Phe Ser Tyr Ile Leu Val Tyr Arg Arg Phe Leu  
 1 5 10 15  
 Phe Val Val Phe Thr Val Leu Val Leu Pro Leu Pro Ile Val Leu  
 20 25 30  
 His Thr Lys Glu Ala Glu Cys Ala Tyr Thr Leu Phe Val Val Ala Thr  
 35 40 45  
 Phe Trp Leu Thr Glu Ala Leu Pro Leu Ser Val Thr Ala Leu Leu Pro  
 50 55 60  
 Ser Leu Met Leu Pro Met Phe Gly Ile Met Pro Ser Lys Lys Val Ala  
 65 70 75 80  
 Ser Ala Tyr Phe Lys Asp Phe His Leu Leu Ile Gly Val Ile Cys

## 4883-0001 substitute.txt

```

      85      90      95
Leu Ala Thr Ser Ile Glu Lys Trp Asn Leu His Lys Arg Ile Ala Leu
      100      105      110
Lys Met Val Met Val Gly Val Asn Pro Ala Trp Leu Thr Leu Gly
      115      120      125
Phe Met Ser Ser Thr Ala Phe Leu Ser Met Trp Leu Ser Asn Thr Ser
      130      135      140
Thr Ala Ala Met Val Met Pro Ile Ala Glu Ala Val Val Gln Gln Ile
      145      150      155
Ile Asn Ala Glu Ala Glu Val Glu Ala Thr Gln Met Thr Tyr Phe Asn
      160      165      170
Gly Ser Thr Asn His Gly Leu Glu Ile Asp Glu Ser Val Asn Gly His
      175      180      185
Glu Ile Asn Glu Arg Lys Glu Lys Thr Lys Pro Val Pro Gly Tyr Asn
      190      195      200
Asn Asp Thr Gly Lys Ile Ser Lys Val Glu Leu Glu Lys Thr Val
      205      210      215

```

&lt;210&gt; SEQ ID NO 47

&lt;211&gt; LENGTH: 88

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 47

```

Ala Thr Gln Met Thr Tyr Phe Asn Gly Ser Thr Asn His Gly Leu Glu
1      5      10      15
Ile Asp Glu Ser Val Asn Gly His Glu Ile Asn Glu Arg Lys Glu Lys
      20      25      30
Thr Lys Pro Val Pro Gly Tyr Asn Asn Asp Thr Gly Lys Ile Ser Ser
      35      40      45
Lys Val Glu Leu Glu Lys His Trp Lys Leu Ala Val Gln Asp Gly Ser
      50      55      60
Pro Ser Pro Ser Val His Ser Val Ser Gln Leu Ala Ala Gln Gly Lys
65      70      75      80
Glu Lys Val Glu Gly Ile Cys Thr
      85

```

&lt;210&gt; SEQ ID NO 48

&lt;211&gt; LENGTH: 112

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 48

```

His Gly Leu Glu Ile Asp Glu Ser Val Asn Gly His Glu Ile Asn Glu
1      5      10      15
Arg Lys Glu Lys Thr Lys Pro Val Pro Gly Tyr Asn Asn Asp Thr Gly
      20      25      30
Lys Ile Ser Ser Lys Val Glu Leu Glu Lys Asn Ser Gly Met Arg Thr
      35      40      45
Lys Tyr Arg Thr Lys Lys Gly His Val Thr Arg Lys Leu Thr Cys Leu
      50      55      60
Cys Ile Ala Tyr Ser Ser Thr Ile Gly Gly Leu Thr Thr Ile Thr Gly
65      70      75      80
Thr Ser Thr Asn Leu Ile Phe Ala Glu Tyr Phe Asn Thr Phe His Pro
      85      90      95
His Arg Arg Gly Asp Arg Thr Arg His Val His Gln Glu Ala Glu Ile
      100      105      110

```

&lt;210&gt; SEQ ID NO 49

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide

&lt;400&gt; SEQUENCE: 49

ccagctttaa ccatgtcaat g

21

<210> SEQ ID NO 50  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <210> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 50  
 cagatggttg tgaggagtct g

21

<210> SEQ ID NO 51  
 <211> LENGTH: 3311  
 <212> TYPE: DNA  
 <213> ORGANISM: Homo sapiens  
 <400> SEQUENCE: 51

tgctaagtct	tttgggtacaa	atggatgtgg	aatataattg	aatatatttct	tgtttaaggg	60
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## 4883-0001 substitute.txt

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
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## 4883-0001 substitute.txt

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<210> SEQ ID NO 53  
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 <212> TYPE: DNA  
 <213> ORGANISM: Homo sapiens  
 <400> SEQUENCE: 53

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## 4883-0001 substitute.txt

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&lt;210&gt; SEQ ID NO 55

&lt;211&gt; LENGTH: 1049

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 55

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&lt;213&gt; ORGANISM: Homo sapiens

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gagtttgaga	agaaggaccg	gacataccca	gtgggagaga	aacttcgcaa	tgctctcaga	240
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## 4883-0001 substitute.txt

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## 4883-0001 substitute.txt

attgcttttc	tgtgaattca	ttagtccatc	tggctgcca	tggaaactca	aacttggaa	4140
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&lt;210&gt; SEQ ID NO 57

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&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Homo sapiens

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<211> LENGTH: 1324
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1324

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
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683

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<211> LENGTH: 914
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
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20 25 30
Glu Gly Ile Val Val Ala Ile Asp Pro Asn Val Pro Glu Asp Glu Thr
35 40 45
Leu Ile Gln Gln Ile Lys Asp Met Val Thr Gln Ala Ser Leu Tyr Leu
50 55 60
Phe Glu Ala Thr Gly Lys Arg Phe Tyr Phe Lys Asn Val Ala Ile Leu
65 70 75 80
Ile Pro Glu Thr Trp Lys Thr Lys Ala Asp Tyr Val Arg Pro Lys Leu

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Glu	Thr	Tyr	Lys 100	Asn	Ala	Asp	Val	Leu 105	Val	Ala	Glu	Ser	Thr 110	Pro	Pro
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Gly	Glu 130	Arg	Ile	His	Leu	Thr 135	Pro	Asp	Phe	Ile	Ala 140	Gly	Lys	Lys	Leu
Ala 145	Glu	Tyr	Gly	Pro	Gln 150	Gly	Lys	Ala	Phe	Val 155	His	Glu	Trp	Ala	His 160
Leu	Arg	Trp	Gly	Val 165	Phe	Asp	Glu	Tyr	Asn 170	Asn	Asp	Glu	Lys	Phe 175	Tyr
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Arg	Cys 210	Thr	Phe	Asn	Lys	Val 215	Thr	Gly	Leu	Tyr	Glu 220	Lys	Gly	Cys	Glu
Phe 225	Val	Leu	Gln	Ser	Arg 230	Gln	Thr	Glu	Lys	Ala 235	Ser	Ile	Met	Phe	Ala 240
Gln	His	Val	Asp	Ser 245	Ile	Val	Glu	Phe	Cys 250	Thr	Glu	Gln	Asn	His 255	Asn
Lys	Glu	Ala	Pro 260	Asn	Lys	Gln	Asn	Gln 265	Lys	Cys	Asn	Leu	Arg 270	Ser	Thr
Trp	Glu	Val 275	Ile	Arg	Asp	Ser	Glu 280	Asp	Phe	Lys	Lys	Thr 285	Thr	Pro	Met
Thr	Thr 290	Gln	Pro	Pro	Asn	Pro 295	Thr	Phe	Ser	Leu	Leu 300	Gln	Ile	Gly	Gln
Arg 305	Ile	Val	Cys	Leu	Val 310	Leu	Asp	Lys	Ser	Gly 315	Ser	Met	Ala	Thr	Gly 320
Asn	Arg	Leu	Asn	Arg 325	Gly	Ser	Trp	Val	Gly 330	Met	Val	Thr	Phe	Asp 335	Ala
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Ala	His	Val 355	Leu	Ser	Glu	Leu	Ile 360	Gln	Met	Asn	Ser	Gly 365	Gly	Thr	Ser
Asp	Thr 370	Leu	Ala	Lys	Arg	Leu 375	Pro	Ala	Ala	Ala	Ser 380	Gly	Gly	Thr	Ser
Ile 385	Cys	Ser	Gly	Leu	Arg 390	Ser	Ala	Phe	Thr	Val 395	Ile	Arg	Lys	Lys	Tyr 400
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Thr	Ile	Ser	Gly 420	Cys	Phe	Asn	Glu	Val 425	Lys	Gln	Ser	Gly	Ala 430	Ile	Ile
His	Thr	Val 435	Ala	Leu	Gly	Pro	Ser 440	Ala	Ala	Gln	Glu	Leu 445	Glu	Glu	Leu
Ser	Lys 450	Met	Thr	Gly	Gly	Leu 455	Gln	Thr	Tyr	Ala	Ser 460	Asp	Gln	Val	Gln
Asn 465	Asn	Gly	Leu	Ile	Asp 470	Ala	Phe	Gly	Ala	Leu 475	Ser	Ser	Gly	Asn	Gly 480
Ala	Val	Ser	Gln	Arg 485	Ser	Ile	Gln	Leu	Glu 490	Ser	Lys	Gly	Leu	Thr 495	Leu
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Gly	Lys	Asp 515	Thr	Leu	Phe	Leu	Ile 520	Thr	Trp	Thr	Thr	Gly 525	Pro	Pro	Gln
Ile	Leu 530	Leu	Trp	Asp	Pro	Ser 535	Gly	Gln	Lys	Gln	Gly 540	Gly	Phe	Val	Val
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Val	Gly	Thr	Trp	Lys 565	Tyr	Ser	Leu	Gln	Ala 570	Ser	Ser	Gln	Thr	Leu 575	Thr
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## 4883-0001 substitute.txt

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Val Val Tyr Ala Asn Ile Arg Gln Gly Ala Ser Ile Leu Arg Ala
610 615 620
Ser Val Thr Ala Leu Ile Glu Ser Val Asn Gly Lys Thr Val Thr Leu
625 630 635 640
Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ala Thr Lys Asp Asp Gly
645 650 655
Val Tyr Ser Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr Ser
660 665 670
Val Lys Val Arg Ala Leu Gly Gly Val Asn Ala Ala Arg Arg Arg Val
675 680 685
Ile Pro Gln Gln Ser Gly Ala Leu Tyr Ile Pro Gly Trp Ile Glu Asn
690 695 700
Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile Asn Lys Asp Asp
705 710 715 720
Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser Ser Gly Gly Ser
725 730 735
Phe Val Ala Ser Asp Val Pro Asn Ala Pro Ile Pro Asp Leu Phe Pro
740 745 750
Pro Gly Gln Ile Thr Asp Leu Lys Ala Glu Ile His Gly Gly Ser Leu
755 760 765
Ile Asn Leu Thr Trp Thr Ala Pro Gly Asp Asp Tyr Asp His Gly Thr
770 775 780
Ala His Lys Tyr Ile Ile Arg Ile Ser Thr Ser Ile Leu Asp Leu Arg
785 790 795 800
Asp Lys Phe Asn Glu Ser Leu Gln Val Asn Thr Thr Ala Leu Ile Pro
805 810 815
Lys Glu Ala Asn Ser Glu Glu Val Phe Leu Phe Lys Pro Glu Asn Ile
820 825 830
Thr Phe Glu Asn Gly Thr Asp Leu Phe Ile Ala Ile Gln Ala Val Asp
835 840 845
Lys Val Asp Leu Lys Ser Glu Ile Ser Asn Ile Ala Arg Val Ser Leu
850 855 860
Phe Ile Pro Pro Gln Thr Pro Pro Glu Thr Pro Ser Pro Asp Glu Thr
865 870 875 880
Ser Ala Pro Cys Pro Asn Ile His Ile Asn Ser Thr Ile Pro Gly Ile
885 890 895
His Ile Leu Lys Ile Met Trp Lys Trp Ile Gly Glu Leu Gln Leu Ser
900 905 910
Ile Ala

```

&lt;210&gt; SEQ ID NO 61

&lt;211&gt; LENGTH: 501

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 61

```

Met Lys Lys Lys Glu Gly Arg Lys Arg Trp Lys Arg Lys Glu Asp Lys Lys
1 5 10 15
Arg Val Val Val Ser Asn Leu Leu Phe Glu Gly Trp Ser His Lys Glu
20 25 30
Asn Pro Asn Arg His His Arg Gly Asn Gln Ile Lys Thr Ser Lys Tyr
35 40 45
Thr Val Leu Ser Phe Val Pro Lys Asn Ile Phe Glu Gln Leu His Arg
50 55 60
Phe Ala Asn Leu Tyr Phe Val Gly Ile Ala Val Leu Asn Phe Ile Pro
65 70 75 80
Val Val Asn Ala Phe Gln Pro Glu Val Ser Met Ile Pro Ile Cys Val
85 90 95
Ile Leu Ala Val Thr Ala Ile Lys Asp Ala Trp Glu Asp Leu Arg Arg
100 105 110
Tyr Lys Ser Asp Lys Val Ile Asn Asn Arg Glu Cys Leu Ile Tyr Ser
115 120 125

```

4883-0001 substitute.txt

Arg	Lys	Glu	Gln	Thr	Tyr	Val	Gln	Lys	Cys	Trp	Lys	Asp	Val	Arg	Val
130						135				140					
Gly	Asp	Phe	Ile	Gln	Met	Lys	Cys	Asn	Glu	Ile	Val	Pro	Ala	Asp	Ile
145					150				155					160	
Leu	Leu	Leu	Phe	Ser	Ser	Asp	Pro	Asn	Gly	Ile	Cys	His	Leu	Glu	Thr
				165					170					175	
Ala	Ser	Leu	Asp	Gly	Glu	Thr	Asn	Leu	Lys	Gln	Arg	Arg	Val	Val	Lys
			180					185					190		
Gly	Phe	Ser	Gln	Gln	Glu	Val	Gln	Phe	Glu	Pro	Glu	Leu	Phe	His	Asn
		195					200					205			
Thr	Ile	Val	Cys	Glu	Lys	Pro	Asn	Asn	His	Leu	Asn	Lys	Phe	Lys	Gly
	210					215					220				
Tyr	Met	Glu	His	Pro	Asp	Gln	Thr	Arg	Thr	Gly	Phe	Gly	Cys	Glu	Ser
225					230					235				240	
Leu	Leu	Leu	Arg	Gly	Cys	Thr	Ile	Arg	Asn	Thr	Glu	Met	Ala	Val	Gly
				245					250					255	
Ile	Val	Ile	Tyr	Ala	Gly	His	Glu	Thr	Lys	Ala	Met	Leu	Asn	Asn	Ser
			260					265					270		
Gly	Pro	Arg	Tyr	Lys	Arg	Ser	Lys	Ile	Glu	Arg	Arg	Met	Asn	Ile	Asp
		275					280					285			
Ile	Phe	Phe	Cys	Ile	Gly	Ile	Leu	Ile	Leu	Met	Cys	Leu	Ile	Gly	Ala
		290				295					300				
Val	Gly	His	Ser	Ile	Trp	Asn	Gly	Thr	Phe	Glu	Glu	His	Pro	Pro	Phe
305					310					315				320	
Asp	Val	Pro	Asp	Ala	Asn	Gly	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Gly	Gly
				325					330					335	
Phe	Tyr	Met	Phe	Leu	Thr	Met	Ile	Ile	Leu	Leu	Gln	Val	Leu	Ile	Pro
				340				345					350		
Ile	Ser	Leu	Tyr	Val	Ser	Ile	Glu	Leu	Val	Lys	Leu	Gly	Gln	Val	Phe
		355					360					365			
Phe	Leu	Ser	Asn	Asp	Leu	Asp	Tyr	Asp	Glu	Glu	Thr	Asp	Leu	Ser	
		370				375				380					
Ile	Gln	Cys	Arg	Ala	Leu	Asn	Ile	Ala	Glu	Asp	Leu	Gly	Gln	Ile	Gln
385					390					395				400	
Tyr	Ile	Phe	Ser	Asp	Lys	Thr	Gly	Thr	Leu	Thr	Glu	Asn	Lys	Met	Val
				405					410					415	
Phe	Arg	Arg	Cys	Thr	Ile	Met	Gly	Ser	Glu	Tyr	Ser	His	Gln	Glu	Asn
			420					425					430		
Gly	Ile	Glu	Ala	Pro	Lys	Gly	Ser	Ile	Pro	Leu	Ser	Lys	Arg	Lys	Tyr
		435					440					445			
Pro	Ala	Leu	Leu	Arg	Asn	Glu	Glu	Ile	Lys	Asp	Ile	Leu	Leu	Ala	Leu
		450				455					460				
Leu	Glu	Ala	Val	Trp	His	Phe	His	Lys	Leu	Pro	Val	Ser	Leu	Trp	
465					470					475				480	
Ser	Ser	Leu	Ser	Gln	Ile	Arg	Ala	Val	Pro	Ile	Thr	Cys	Lys	Leu	Ser
				485					490					495	
Phe	Val	Tyr	Lys	Gly											
			500												

<210> SEQ ID NO 62

<211> LENGTH: 154

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

Met	Gly	Arg	Arg	Ser	Pro	Phe	Lys	Pro	Arg	Asn	Lys	Val	Phe	Gly	Phe
1				5					10				15		
Ser	Tyr	Pro	Trp	Cys	Arg	Ser	Tyr	Gln	Pro	Phe	Pro	Arg	Lys	Arg	Ala
			20					25					30		
Trp	Pro	Pro	Ser	Arg	Val	Trp	Leu	Gly	Ala	Cys	Cys	Ala	Ser	Leu	Ala
			35				40					45			
Ser	Pro	Pro	Lys	Gly	Thr	Ile	Pro	Ser	Gly	Glu	Tyr	Tyr	Arg	Pro	Ala
	50					55				60					
Pro	Ser	Ser	Ser	Gly	Asp	Ser	Leu	Arg	Arg	Glu	Ser	Gly	Ala	Leu	Leu

## 4883-0001 substitute.txt

```

65      70      75      80
Gln Tyr Leu Pro Ser Leu Ala Ser Pro Cys Ala Asn His Ala Thr Arg
      85
Cys Ser Leu Leu Phe Pro Ile Tyr Lys Ile Lys Met Thr Leu Tyr
      100
Leu Thr Gly Leu Ala Arg Thr His Cys Cys Leu Ala Asp Arg Cys
      115
Ala Glu Ala Val Glu Ser Ala Phe Tyr Leu Val Gly Ser Leu Cys Ile
      130
Asn Ala Arg Gly Ala Ala His Leu Thr Asp
      145      150

```

&lt;210&gt; SEQ ID NO 63

&lt;211&gt; LENGTH: 484

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 63

```

Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala Ala
1      5      10      15
Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile Leu Gly
      20      25      30
Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys Asp His Asn
      35      40      45
Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser Ala Met Arg Glu
      50      55      60
Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser Leu Val Asn Thr Val
65      70      75      80
Leu Lys His Ile Ile Trp Leu Lys Val Ile Thr Ala Asn Ile Leu Gln
      85      90      95
Leu Gln Val Lys Pro Ser Ala Asn Asp Gln Glu Leu Leu Val Lys Ile
      100      105      110
Pro Leu Asp Met Val Ala Gly Phe Asn Thr Pro Leu Val Lys Thr Ile
      115      120      125
Val Glu Phe His Met Thr Thr Glu Ala Gln Ala Thr Ile Arg Met Asp
      130      135      140
Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr
145      150      155      160
Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu
      165      170      175
Val Asn Ala Leu Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu
      180      185      190
Pro Asn Leu Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe
      195      200      205
Asn Gly Met Tyr Ala Asp Leu Gln Leu Val Lys Val Pro Ile Ser
      210      215      220
Leu Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
225      230      235      240
Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser Gln
      245      250      255
Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu Thr Met
      260      265      270
Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser Gln Asp Val
      275      280      285
Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu Glu Phe Met Val
      290      295      300
Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His Arg Leu Lys Ser Ser
305      310      315      320
Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp Lys Leu Gly Ser Thr Gln
      325      330      335
Ile Val Lys Ile Leu Thr Gln Asp Thr Pro Glu Phe Ile Asp Gln
      340      345      350
Gly His Ala Lys Val Ala Gln Ile Val Leu Glu Val Phe Pro Ser
      355      360      365

```

4883-0001 substitute.txt

Ser	Glu	Ala	Leu	Arg	Pro	Leu	Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser
370						375					380				
Glu	Ala	Gln	Phe	Tyr	Thr	Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn
385					390					395				400	
Asn	Ile	Ser	Ser	Asp	Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp
				405					410					415	
Phe	Gln	Pro	Asp	Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser
			420						425					430	
Ile	Leu	Leu	Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val
		435					440					445			
Ser	Leu	Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr
	450					455					460				
Lys	Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser
465					470					475				480	
Pro	Val	Ser	Gln												

<210> SEQ ID NO 64

<211> LENGTH: 256

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

Met	Phe	Gln	Thr	Gly	Gly	Leu	Ile	Val	Phe	Tyr	Gly	Leu	Leu	Ala	Gln
1				5					10					15	
Thr	Met	Ala	Gln	Phe	Gly	Gly	Leu	Pro	Val	Pro	Leu	Asp	Gln	Thr	Leu
			20					25					30		
Pro	Leu	Asn	Val	Asn	Pro	Ala	Leu	Pro	Leu	Ser	Pro	Thr	Gly	Leu	Ala
		35					40					45			
Gly	Ser	Leu	Thr	Asn	Ala	Leu	Ser	Asn	Gly	Leu	Leu	Ser	Gly	Gly	Leu
	50					55					60				
Leu	Gly	Ile	Leu	Glu	Asn	Leu	Pro	Leu	Leu	Asp	Ile	Leu	Lys	Pro	Gly
65					70				75					80	
Gly	Gly	Thr	Ser	Gly	Gly	Leu	Leu	Gly	Gly	Leu	Leu	Gly	Lys	Val	Thr
				85					90					95	
Ser	Val	Ile	Pro	Gly	Leu	Asn	Asn	Ile	Ile	Asp	Ile	Lys	Val	Thr	Asp
			100					105					110		
Pro	Gln	Leu	Leu	Glu	Leu	Gly	Leu	Val	Gln	Ser	Pro	Asp	Gly	His	Arg
		115					120					125			
Leu	Tyr	Val	Thr	Ile	Pro	Leu	Gly	Ile	Lys	Leu	Gln	Val	Asn	Thr	Pro
		130					135					140			
Leu	Val	Gly	Ala	Ser	Leu	Leu	Arg	Leu	Ala	Val	Lys	Leu	Asp	Ile	Thr
145					150					155					
Ala	Glu	Ile	Leu	Ala	Val	Arg	Asp	Lys	Gln	Glu	Arg	Ile	His	Leu	Val
				165						170				175	
Leu	Gly	Asp	Cys	Thr	His	Ser	Pro	Gly	Ser	Leu	Gln	Ile	Ser	Leu	Leu
			180					185					190		
Asp	Gly	Leu	Gly	Pro	Leu	Pro	Ile	Gln	Gly	Leu	Leu	Asp	Ser	Leu	Thr
		195					200					205			
Gly	Ile	Leu	Asn	Lys	Val	Leu	Pro	Glu	Leu	Val	Gln	Gly	Asn	Val	Cys
		210					215				220				
Pro	Leu	Val	Asn	Glu	Val	Leu	Arg	Gly	Leu	Asp	Ile	Thr	Leu	Val	His
225					230					235				240	
Asp	Ile	Val	Asn	Met	Leu	Ile	His	Gly	Leu	Gln	Phe	Val	Ile	Lys	Val
				245					250					255	

<210> SEQ ID NO 65

<211> LENGTH: 791

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

Met	Ser	Gln	Pro	Arg	Pro	Arg	Tyr	Val	Val	Asp	Arg	Ala	Ala	Tyr	Ser
1				5					10					15	
Leu	Thr	Leu	Phe	Asp	Asp	Glu	Phe	Glu	Lys	Lys	Asp	Arg	Thr	Tyr	Pro
			20					25					30		



## 4883-0001 substitute.txt

Val	Gly	Glu	Lys	Leu	Arg	Asn	Ala	Phe	Arg	Cys	Ser	Ser	Ala	Lys	Ile
		35					40				45				
Lys	Ala	Val	Val	Phe	Gly	Leu	Leu	Pro	Val	Leu	Ser	Trp	Leu	Pro	Lys
		50				55				60					
Tyr	Lys	Ile	Lys	Asp	Tyr	Ile	Ile	Pro	Asp	Leu	Leu	Gly	Gly	Leu	Ser
65					70				75					80	
Gly	Gly	Ser	Ile	Gln	Val	Pro	Gln	Gly	Met	Ala	Phe	Ala	Leu	Leu	Ala
				85					90				95		
Asn	Leu	Pro	Ala	Val	Asn	Gly	Leu	Tyr	Ser	Ser	Phe	Phe	Pro	Leu	Leu
			100					105					110		
Thr	Tyr	Phe	Phe	Leu	Gly	Gly	Val	His	Gln	Met	Val	Pro	Gly	Thr	Phe
		115					120					125			
Ala	Val	Ile	Ser	Ile	Leu	Val	Gly	Asn	Ile	Cys	Leu	Gln	Leu	Ala	Pro
		130				135					140				
Glu	Ser	Lys	Phe	Gln	Val	Phe	Asn	Asn	Ala	Thr	Asn	Glu	Ser	Tyr	Val
145					150				155						160
Asp	Thr	Ala	Ala	Met	Glu	Ala	Glu	Arg	Leu	His	Val	Ser	Ala	Thr	Leu
				165					170					175	
Ala	Cys	Leu	Thr	Ala	Ile	Ile	Gln	Met	Gly	Leu	Gly	Phe	Met	Gln	Phe
			180					185					190		
Gly	Phe	Val	Ala	Ile	Tyr	Leu	Ser	Glu	Ser	Phe	Ile	Arg	Gly	Phe	Met
		195					200					205			
Thr	Ala	Ala	Gly	Leu	Gln	Ile	Leu	Ile	Ser	Val	Leu	Lys	Tyr	Ile	Phe
		210				215					220				
Gly	Leu	Thr	Ile	Pro	Ser	Tyr	Thr	Gly	Pro	Gly	Ser	Ile	Val	Phe	Thr
225					230					235					240
Phe	Ile	Asp	Ile	Cys	Lys	Asn	Leu	Pro	His	Thr	Asn	Ile	Ala	Ser	Leu
				245					250					255	
Ile	Phe	Ala	Leu	Ile	Ser	Gly	Ala	Phe	Leu	Val	Leu	Val	Lys	Glu	Leu
			260					265					270		
Asn	Ala	Arg	Tyr	Met	His	Lys	Ile	Arg	Phe	Pro	Ile	Pro	Thr	Glu	Met
		275					280					285			
Ile	Val	Val	Val	Val	Ala	Thr	Ala	Ile	Ser	Gly	Gly	Cys	Lys	Met	Pro
		290				295					300				
Lys	Lys	Tyr	His	Met	Gln	Ile	Val	Gly	Glu	Ile	Gln	Arg	Gly	Phe	Pro
305					310				315						320
Thr	Pro	Val	Ser	Pro	Val	Val	Ser	Gln	Trp	Lys	Asp	Met	Ile	Gly	Thr
				325					330					335	
Ala	Phe	Ser	Leu	Ala	Ile	Val	Ser	Tyr	Val	Ile	Asn	Leu	Ala	Met	Gly
			340					345				350			
Arg	Thr	Leu	Ala	Asn	Lys	His	Gly	Tyr	Asp	Val	Asp	Ser	Asn	Gln	Glu
		355					360					365			
Met	Ile	Ala	Leu	Gly	Cys	Ser	Asn	Phe	Phe	Gly	Ser	Phe	Phe	Lys	Ile
		370				375					380				
His	Val	Ile	Cys	Cys	Ala	Leu	Ser	Val	Thr	Leu	Ala	Val	Asp	Gly	Ala
385					390					395					400
Gly	Gly	Lys	Ser	Gln	Val	Ala	Ser	Leu	Cys	Val	Ser	Leu	Val	Val	Met
				405					410					415	
Ile	Thr	Met	Leu	Val	Leu	Gly	Ile	Tyr	Leu	Tyr	Pro	Leu	Pro	Lys	Ser
			420					425					430		
Val	Leu	Gly	Ala	Leu	Ile	Ala	Val	Asn	Leu	Lys	Asn	Ser	Leu	Lys	Gln
		435					440					445			
Leu	Thr	Asp	Pro	Tyr	Tyr	Leu	Trp	Arg	Lys	Ser	Lys	Leu	Asp	Cys	Cys
		450				455					460				
Ile	Trp	Val	Val	Ser	Phe	Leu	Ser	Ser	Phe	Phe	Leu	Ser	Leu	Pro	Tyr
465					470				475						480
Gly	Val	Ala	Val	Gly	Val	Ala	Phe	Ser	Val	Leu	Val	Val	Val	Phe	Gln
				485					490					495	
Thr	Gln	Phe	Arg	Asn	Gly	Tyr	Ala	Leu	Ala	Gln	Val	Met	Asp	Thr	Asp
			500					505					510		
Ile	Tyr	Val	Asn	Pro	Lys	Thr	Tyr	Asn	Arg	Ala	Gln	Asp	Ile	Gln	Gly
		515					520					525			
Ile	Lys	Ile	Ile	Thr	Tyr	Cys	Ser	Pro	Leu	Tyr	Phe	Ala	Asn	Ser	Glu

## 4883-0001 substitute.txt

```

      530
Ile Phe Arg Gln Lys Val 535
545 Val Leu Leu Ala Lys 550
      565
Met Arg Pro Thr Gln Arg Arg Ser Leu Phe Met Lys Thr Thr
      580
Val Ser Leu Gln Glu Leu Gln Gln Asp Phe Glu Asn Ala Pro Pro Thr
      595
Asp Pro Asn Asn Asn Gln Thr 600
      610
Ile Thr Phe Ser Pro Asp Ser Ser Pro Ala Gln Ser Glu Pro Pro
      625
Ala Ser Ala Glu Ala 630
      645
Pro Pro Phe Val Thr Phe His Thr Leu Ile Leu Asp Met Ser Gly Val
      660
Ser Phe Val Asp Leu Met Gly Ile Lys Ala Leu Ala Lys Leu Ser Ser
      675
Thr Tyr Gly Lys Ile Gly Val Lys Val Phe Leu Val Asn Ile His Ala
      690
Gln Val Tyr Asn Asp Ile Ser His Gly Gly Phe Glu Asp Gly Ser
      705
Leu Glu Cys Lys His Val Phe Pro Ser Ile His Asp Ala Val Leu Phe
      720
Ala Gln Ala Asn Ala Arg Asp Val Thr Pro Gly His Asn Phe Gln Gly
      740
Ala Pro Gly Asp Ala Glu Leu Ser Leu Tyr Asp Ser Glu Glu Asp Ile
      755
Arg Ser Tyr Trp Asp Leu Glu Gln Glu Met Phe Gly Ser Met Phe His
      770
Ala Glu Thr Leu Thr Ala Leu
      785
      790

```

&lt;210&gt; SEQ ID NO 66

&lt;211&gt; LENGTH: 243

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 66

```

Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro Val Asn Val Phe
1      5
Ser Val Thr Pro Tyr Thr Pro Ser Thr Ala Asp Ile Gln Val Ser Asp
      20
Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly Ile Phe Leu Gly
      35
Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile Lys Tyr Gln Gly
      50
Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro Val Leu Leu Ser
      65
Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys Phe Lys Met Leu
      85
Ser Cys Gln Leu Cys Lys Glu Ser Glu Arg Val Pro Asp Ser Glu
      100
Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly Ile Asn Gln Pro
      115
Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile Pro Pro Pro Tyr
      130
Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr Leu Gln Ser Val
      145
Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Ala Ala Ala Ala Met
      165
Ser Ser Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln Asp Asn Ser Ala
      180
      185
      190

```

4883-0001 substitute.txt

Phe	Val	Val	Asp	Glu	Gly	Cys	Leu	Ser	Phe	Thr	Asp	Gly	Gly	Asn	His
		195					200					205			
Arg	Pro	Asn	Pro	Asp	Val	Asp	Gln	Leu	Glu	Glu	Thr	Gln	Leu	Glu	Glu
	210					215					220				
Glu	Ala	Cys	Ala	Cys	Phe	Ser	Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Tyr	Ser
225					230					235					240
Leu	Pro	Arg													

<210> SEQ ID NO 67  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 67  
 acacgaatgg tagatacagt g 21

<210> SEQ ID NO 68  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 68  
 atacttgta gctgttccat g 21

<210> SEQ ID NO 69  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 69  
 actgttacct tgcattgact g 21

<210> SEQ ID NO 70  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 70  
 caatgagaac acatggacat g 21

<210> SEQ ID NO 71  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 71  
 ccatgaaagc tccatgtcta c 21

<210> SEQ ID NO 72  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 72  
 agataggca catattctgt c 21

<210> SEQ ID NO 73

```

<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 73
    atcggctgaa gtcaagcatc g                                21

<210> SEQ ID NO 74
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 74
    tggtcagtga ggactcagct g                                21

<210> SEQ ID NO 75
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 75
    tttctctgct tgatgcactt g                                21

<210> SEQ ID NO 76
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 76
    gtgagcactg ggaagcagct c                                21

<210> SEQ ID NO 77
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 77
    ggcaaatgct agagacgtga c                                21

<210> SEQ ID NO 78
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 78
    aggtgtcctt cagtgccaa g                                21

<210> SEQ ID NO 79
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 79
    gttaagtgtc ctctggattt g                                21

<210> SEQ ID NO 80

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<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 80
    atcctgattg ctgtgtgcaa g                                21

<210> SEQ ID NO 81
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 81
    ctcttctagc tggtaacat c                                21

<210> SEQ ID NO 82
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 82
    ccagcaacaa cttacgtggt c                                21

<210> SEQ ID NO 83
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 83
    cttttattca cccaatcact c                                21

<210> SEQ ID NO 84
<211> LENGTH: 2165
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 84
    agaacagcgc agtttgcctt ccgctcacgc agagcctctc cgtggcctcc gcaccttgag      60
    cattaggcca gtctctctct tctctctaatt ccatccgtca cctctctctgt catccgtttc      120
    catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt ttggttctga      180
    gtctctctcaa gctgggatca gggcagtggt aggtgtttgg gccagacaag cctgtccagg      240
    ccttggtggg ggaggacgca gcattctctct gtttctctgt tcttaagacc aatgcagagg      300
    ccattggaagt gcggttcttc aggggccagt tctctagcgt ggtccacctc tacaggggacg      360
    ggaaggacca gccatttatg cagatgccac agtatcaagg caggacaaaa ctgggtgaagg      420
    attctattgc ggaggggcgc atctctctga ggcctggaata cattactgtg ttggatgctg      480
    gccctctatgg gtgcaggatt agttcccgagt cttactacca gaaggccatc tgggagctac      540
    aggtgtcagc actgggctca gtctctctca ttcccatcac agacatgcat ggaatattgt      600
    tcagctactc ctgtcagtcg tcgggctggt tccccgggcc cacagcgaag tggaaaggctc      660
    cacaaggaca ggattttgct acagactcca ggacaacac agacatgcat ggcctgtttg      720
    atgtggagat ctctctgacc gtccaagaga acgcccggag catatccgtg tccatgcggc      780
    atgctcatct gaggccgagag gtggaatcca gggtaacagt aggagatacc ttttccgagc      840
    ctatatctgt gcacctggct accaaagtac tgggaatact ctgctgtggc ctattttttg      900
    gcattgttgg actgaagatt ttcttctcca aattccagtg taagcgagag agagaagcat      960
    gggccgggtgc cttattcatg gttccagcag ggacaggatc agagatgcct ccacatccag      1020
    ctgcttctct tcttctagtc ctagcctcca ggggccagg cccaaaaaag gaaaaatccag      1080
    gcggaactgg acttgagaag aaagcacgga caggcagaat tgagagacgc ccggaacac      1140
    cgagtggagg tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg      1200
    aaaactgtaa ccatagaaa agctccccag gaggtgccct actctgagaa gagatttaac      1260
    aggaagagtg tgggtggctc tcagagtttc caagcaggga aacattactg ggaggtggac      1320
    ggaggacaca ataaaagggt gcgcgtggga atgatgtgga caggaggaag      1380

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gagtacgtga	ctttgtctcc	cgatcatggg	tactgggtcc	tcagactgaa	tggagaacat	1440
ttgtatttca	cattaaatcc	cggttttatc	agcgtcttcc	ccaggacccc	acctacaaaa	1500
atagggggtc	tcctgggacta	tgagtgtggg	accatctcct	tcctcaacat	aaatgaccag	1560
tcctcttatt	ataccctgac	atgtcgggtt	gaaggcctta	tgaggcccta	cattgagtat	1620
ccgtctcata	atagacaaaa	tggaactccc	atagtcatct	gccacgtcac	ccaggaatca	1680
gagaaagagg	ccctctggga	aagggcctct	gcaatcccag	agacaagcaa	cagtgaagtc	1740
tcctcacagg	caaccacgcc	cttctctccc	aggggtgaaa	tgtagatgta	atcacatccc	1800
acattcttct	ttagggatat	taagggtctct	ctcccagatc	caaagtcccc	cagcagccgg	1860
ccaaggtggc	ttccagatga	agggggactg	gcctgtccac	atgggagtc	gggtgtcatgg	1920
ctgccttgag	ctgggagggg	agaaggctga	cattacattt	agtttgctct	cactccatct	1980
ggctaagtga	tccttgaata	ccacctctca	ggtagaaga	cgctcagga	tcctcatctca	2040
caggctgtgg	ttagatttaa	gtagacaagg	aattgtgaata	atgtcttagat	cttatttgatg	2100
acagatgtga	tcctaattggt	ttgttcatta	tattacactt	tcagtaaaaa	aaaaaaaaaaa	2160
aaaaa						2165

&lt;210&gt; SEQ ID NO 85

&lt;211&gt; LENGTH: 347

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 85

```

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly Ser
1      5      10      15
Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala Leu Val
20      25
Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys Thr Asn Ala
35      40      45
Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe Ser Ser Val Val
50      55      60
His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe Met Gln Met Pro Gln
65      70      75
Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp Ser Ile Ala Glu Gly Arg
85      90      95
Ile Ser Leu Arg Leu Glu Asn Ile Thr Val Leu Asp Ala Gly Leu Tyr
100      105      110
Gly Cys Arg Ile Ser Ser Gln Ser Tyr Tyr Gln Lys Ala Ile Trp Glu
115      120      125
Leu Gln Val Ser Ala Leu Gly Ser Val Pro Leu Ile Ser Ile Thr Gly
130      135      140
Tyr Val Asp Arg Asp Ile Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe
145      150      155
Pro Arg Pro Thr Ala Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser
165      170      175
Thr Asp Ser Arg Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu
180      185      190
Ile Ser Leu Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met
195      200      205
Arg His Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly
210      215      220
Asp Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu
225      230      235
Gly Ile Leu Cys Cys Gly Leu Phe Phe Gly Ile Val Gly Leu Lys Ile
245      250      255
Phe Phe Ser Lys Phe Gln Cys Lys Arg Glu Arg Glu Ala Trp Ala Gly
260      265      270
Ala Leu Phe Met Val Pro Ala Gly Thr Gly Ser Glu Met Leu Pro His
275      280      285
Pro Ala Ala Ser Leu Leu Leu Val Leu Ala Ser Arg Gly Pro Gly Pro
290      295      300
Lys Lys Glu Asn Pro Gly Gly Thr Gly Leu Glu Lys Lys Ala Arg Thr
305      310      315
Gly Arg Ile Glu Arg Arg Pro Glu Thr Arg Ser Gly Gly Asp Ser Gly
320      325      330
Ser Arg Asp Gly Ser Pro Glu Ala Leu Arg Phe
335

```

340

345

<210> SEQ ID NO 86  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 86  
 attcatggtt ccagcagga c 21

<210> SEQ ID NO 87  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 87  
 gggagacaaa gtcacgtact c 21

<210> SEQ ID NO 88  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 88  
 tcctggtgtt cgtggtctgc tt 22

<210> SEQ ID NO 89  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide  
 <400> SEQUENCE: 89  
 gagagtcctg gcttttgtgg gc 22

<210> SEQ ID NO 90  
 <211> LENGTH: 15  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <400> SEQUENCE: 90  
 Gly Ser Ser Asp Leu Thr Trp Pro Pro Ala Ile Lys Leu Gly Cys  
 1 5 10 15

<210> SEQ ID NO 91  
 <211> LENGTH: 16  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <400> SEQUENCE: 91  
 Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg  
 1 5 10 15

<210> SEQ ID NO 92  
 <211> LENGTH: 15  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <400> SEQUENCE: 92  
 Val Ala Pro Arg Ala Lys Ala His Lys Ser Gln Asp Ser Leu Cys  
 1 5 10 15

<210> SEQ ID NO 93

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<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 93
  Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Arg
  1                               5                               10

<210> SEQ ID NO 94
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 94
  Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro
  1                               5                               10                               15
  Pro Ala Ile Lys Leu Gly
  20

<210> SEQ ID NO 95
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 95
  Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly
  1                               5                               10

<210> SEQ ID NO 96
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 96
  Gly Ile Gln Glu Gly Gly Phe Cys Phe Arg Ser Thr Arg His Asn Phe
  1                               5                               10                               15
  Asn Ser Met Arg Phe Pro
  20

<210> SEQ ID NO 97
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 97
  Ala Lys Glu Phe Gln Glu Ala Ser Ala Leu Ala Val Ala Pro Arg Ala
  1                               5                               10                               15
  Lys Ala His Lys Ser Gln Asp Ser Leu Cys Val Thr Leu Ala
  20                               25                               30

<210> SEQ ID NO 98
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 98
  tcctgctcgt cgctctcctg at
  22

<210> SEQ ID NO 99
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 99
  tcgctttttg tcgtatttgc
  20

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<210> SEQ ID NO 100
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 100
His Asn Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser
1 5 10 15

<210> SEQ ID NO 101
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 101
Asn Leu Pro Thr Pro Thr Val Glu Asn Gln Gln Arg Leu Ala
1 5 10 15

<210> SEQ ID NO 102
<211> LENGTH: 619
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 102
Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp Ser His
1 5 10 15
Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu Thr Asn His
20 25 30
Val Ser Leu Lys Ile Asp Asp Lys Arg Arg Asp Thr Ile Gln Arg
35 40 45
Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg Val Ile Leu Lys Asp Leu
50 55 60
Lys His Asn Asp Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu Leu Asn
65 70 75 80
Lys Leu Leu Gln Ile Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr Gly Thr
85 90 95
Val Lys Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg
100 105 110
Gly Ser Leu Arg Glu Val Leu Asn Asp Thr Ile Ser Tyr Pro Asp Gly
115 120 125
Thr Phe Met Asp Trp Glu Phe Lys Ile Ser Val Leu Tyr Asp Ile Ala
130 135 140
Lys Gly Met Ser Tyr Leu His Ser Ser Lys Thr Glu Val His Gly Arg
145 150 155 160
Leu Lys Ser Thr Asn Cys Val Val Asp Ser Arg Met Val Val Lys Ile
165 170 175
Thr Asp Phe Gly Cys Asn Ser Ile Leu Pro Pro Lys Lys Asp Leu Trp
180 185 190
Thr Ala Pro Glu His Leu Arg Gln Ala Asn Ile Ser Gln Lys Gly Asp
195 200 205
Val Tyr Ser Tyr Gly Ile Ile Ala Gln Glu Ile Ile Leu Arg Lys Glu
210 215 220
Thr Phe Tyr Thr Leu Ser Cys Arg Asp Arg Asn Glu Lys Ile Phe Arg
225 230 235 240
Val Glu Asn Ser Asn Gly Met Lys Pro Phe Arg Pro Asp Leu Phe Leu
245 250 255
Glu Thr Ala Glu Lys Lys Glu Leu Glu Val Tyr Leu Leu Val Lys Asn
260 265 270
Cys Trp Glu Glu Asp Pro Glu Lys Arg Pro Asp Phe Lys Lys Ile Glu
275 280 285
Thr Thr Leu Ala Lys Ile Phe Gly Leu Phe His Asp Gln Lys Asn Glu
290 295 300
Ser Tyr Met Asp Thr Leu Ile Arg Arg Leu Gln Leu Tyr Ser Arg Asn
305 310 315 320
Leu Glu His Leu Val Glu Glu Arg Thr Gln Leu Tyr Lys Ala Glu Arg
325 330 335

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Asp Arg Ala Asp Arg Leu Asn Phe Met Leu Leu Pro Arg Leu Val Val
340 345 350
Lys Ser Leu Lys Glu Lys Gly Phe Val Glu Pro Glu Leu Tyr Glu Glu
355 360 365
Val Thr Ile Tyr Phe Ser Asp Ile Val Gly Phe Thr Thr Ile Cys Lys
370 375 380
Tyr Ser Thr Pro Met Glu Val Val Asp Met Leu Asn Asp Ile Tyr Lys
385 390 395
Ser Phe Asp His Ile Val Asp His His Asp Val Tyr Lys Val Glu Thr
400 405 410 415
Ile Gly Asp Ala Tyr Met Val Ala Ser Gly Leu Pro Lys Arg Asn Gly
420 425 430
Asn Arg His Ala Ile Asp Ile Ala Lys Met Ala Leu Glu Ile Leu Ser
435 440 445
Phe Met Gly Thr Phe Glu Leu Glu His Leu Pro Gly Leu Pro Ile Trp
450 455 460
Ile Arg Ile Gly Val His Ser Gly Pro Cys Ala Ala Gly Val Val Gly
465 470 475 480
Ile Lys Met Pro Arg Tyr Cys Leu Phe Gly Asp Thr Val Asn Thr Ala
485 490 495
Ser Arg Met Glu Ser Thr Gly Leu Pro Leu Arg Ile His Val Ser Gly
500 505 510
Ser Thr Ile Ala Ile Leu Lys Arg Thr Glu Cys Gln Phe Leu Tyr Glu
515 520 525
Val Arg Gly Glu Thr Tyr Leu Lys Gly Arg Gly Asn Glu Thr Thr Tyr
530 535 540
Trp Leu Thr Gly Met Lys Asp Gln Lys Phe Asn Leu Pro Thr Pro Pro
545 550 555 560
Thr Val Glu Asn Gln Gln Arg Leu Gln Ala Glu Phe Ser Asp Met Ile
565 570 575
Ala Asn Ser Leu Gln Lys Arg Gln Ala Ala Gly Ile Arg Ser Gln Lys
580 585 590
Pro Arg Arg Val Ala Ser Tyr Lys Lys Gly Thr Leu Glu Tyr Leu Gln
595 600 605
Leu Asn Thr Thr Asp Lys Glu Ser Thr Tyr Phe
610 615

```

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<210> SEQ ID NO 103
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 103
gctggttaact atcttcctgc
20

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<210> SEQ ID NO 104
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 104
gaagaatggt gtccagaggt
20

```

```

<210> SEQ ID NO 105
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 105
Leu Ile Asn Lys Val Pro Leu Pro Val Asp Lys Leu Ala Pro Leu
1 5 10 15

```

```

<210> SEQ ID NO 106
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 106
    Ser Glu Ala Val  Lys Lys Leu Leu Glu  Ala Leu Ser His Leu Val
      1              5              10              15

<210> SEQ ID NO 107
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 107
    tgttttcaac taccaggggc
                                     20

<210> SEQ ID NO 108
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 108
    tgttggtttt ggcagagtcc
                                     20

<210> SEQ ID NO 109
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 109
    gaggcagagt tcaggcttca ccga
                                     24

<210> SEQ ID NO 110
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 110
    tgttggtttt ggcagagtcc
                                     20

<210> SEQ ID NO 111
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 111
    Thr Gly Met Asp Met Trp Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val
      1              5              10              15
    Thr Ser Val Phe Gln Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln
      20              25              30
    Ser Ser Gly Phe Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu
      35              40              45
    Pro Ala Met Leu Gln Ala Val Arg
      50              55

<210> SEQ ID NO 112
<211> LENGTH: 53
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 112

```

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Asp Gln Trp Ser Thr Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val  
 1 5 10 15  
 Phe Asn Tyr Gln Gly Leu Trp Arg Ser Cys Val Arg Glu Ser Gly  
 20 25 30  
 Phe Thr Glu Cys Arg Gly Tyr Phe Thr Leu Leu Gly Leu Pro Ala Met  
 35 40 45  
 Leu Gln Ala Val Arg  
 50

&lt;210&gt; SEQ ID NO 113

&lt;211&gt; LENGTH: 14

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 113

Ser Thr Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val Phe  
 1 5 10

&lt;210&gt; SEQ ID NO 114

&lt;211&gt; LENGTH: 12

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 114

Asp Met Trp Ser Thr Gln Asp Leu Tyr Asp Asn Pro  
 1 5 10

&lt;210&gt; SEQ ID NO 115

&lt;211&gt; LENGTH: 12

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 115

Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala  
 1 5 10

&lt;210&gt; SEQ ID NO 116

&lt;211&gt; LENGTH: 13

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 116

Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly  
 1 5 10

&lt;210&gt; SEQ ID NO 117

&lt;211&gt; LENGTH: 816

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 117

gccaggatca	tgtccaccac	cacatgccaa	gtggtggcgt	tcctcctgtc	catcctgggg	60
ctggccggct	gcactgcggc	caccgggatg	gacatgtgga	gcaccagga	cctgtacgac	120
aaccccgcta	ccctcgtggt	ccagtacgaa	gggctctgga	ggagctgcgt	gaggcagagt	180
tcaggcttca	ccgaatgcag	gccctatttc	accatccctg	gacttcagc	catgctgcag	240
gcagtgcgag	ccctgatgat	cgtaggcatc	gtcctggggt	ccattggcct	cctggtatcc	300
atctttgccc	tgaatgcat	cgcatgtggc	agcatggagg	actctgccaa	agccaacatg	360
acactgacct	ccgggatcat	gttcattgtc	tcaggctctt	gtgcaattgc	tggagtgtct	420
gtgtttgcca	acatgctggt	gactaacctc	tggatgtcca	cagctaaccat	gtacaccggc	480
atgggtggga	tgtgtcgagc	tggtcagacc	aggtagacat	ttggtgcggc	tctgttcgtg	540
ggctgggtcg	ctggaggcct	cacactaatt	gggggtgtga	tgatgtgcat	cgccctggcg	600
ggcctggcac	cagaagaaac	caactacaaa	gccgtttctt	atcatgcctc	aggccacagt	660
gttgcttaca	agcctggagg	cttcaaggcc	agcactggct	ttgggtccaa	cacaaaaaac	720
aagaagatat	acgatggagg	tgccccaca	gaggacgagg	tacaatctta	tccttccaag	780
cacgactatg	tgtaatgctc	taagacctct	cagcac			816

&lt;210&gt; SEQ ID NO 118

&lt;211&gt; LENGTH: 261

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```

<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 118
Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1      5      10      15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
20
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
35
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
50
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65      70      75      80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
85
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145      150      155      160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225      230      235      240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245
Lys His Asp Tyr Val
260

```

```

<210> SEQ ID NO 119
<211> LENGTH: 227
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 119
gccaggatca tgtccaccac cacatgccaa gtggtggcgt tctctctgtc catcctgggg      60
ctggccggct gcatcggcgc caccgggatg gacatgtgga gcaccaggga cctgtacgac      120
aaccgccgtc cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt      180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gactttcc      227

```

```

<210> SEQ ID NO 120
<211> LENGTH: 69
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 120
Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1      5      10      15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
20
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
35
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
50
Pro Tyr Phe Thr Ile
55

```

```

<210> SEQ ID NO 121
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 121
aatgagagga aagagaaac
20

<210> SEQ ID NO 122
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 122
atggtagaag ataggcaat
20

<210> SEQ ID NO 123
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 123
Glu Lys Trp Asn Leu His Lys Arg Ile Ala Leu Lys Met Val Cys
1 5 10 15

<210> SEQ ID NO 124
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 124
Cys Leu Gly Phe Asn Phe Lys Glu Met Phe Lys
1 5 10

<210> SEQ ID NO 125
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 125
taatgatgaa ccctacactg agc
23

<210> SEQ ID NO 126
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 126
atggacaaat gccctacctt
20

<210> SEQ ID NO 127
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 127
agtgtctggaa ggatgtgctg gt
22

<210> SEQ ID NO 128

```

## 4883-0001 substitute.txt

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 128
    ttgagggtgtg tgttgggttt
    20

<210> SEQ ID NO 129
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 129
    agatgtgctg aggctgtaga
    20

<210> SEQ ID NO 130
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 130
    atgaaggttg attatttgag
    20

<210> SEQ ID NO 131
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 131
    agccgcatac tcccttacc tct
    23

<210> SEQ ID NO 132
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 132
    gcagcagccc aaacaccaca
    20

<210> SEQ ID NO 133
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 133
    ctgagccgag aggtggaatc
    20

<210> SEQ ID NO 134
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 134
    ctctctcgct tacactggaa
    20

<210> SEQ ID NO 135

```

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<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 135
  Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala Leu
  1                               5                               10

<210> SEQ ID NO 136
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 136
  Ala Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser
  1                               5                               10                               15

<210> SEQ ID NO 137
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 137
  Asn Met Leu Val Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr
  1                               5                               10                               15
  Gly Met Gly Gly Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly
  20                               25                               30

<210> SEQ ID NO 138
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 138
  cgtgagcgct tcgagatggtt ccg                                     23

<210> SEQ ID NO 139
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 139
  cctaaccagc tgcccaactg tag                                     23

<210> SEQ ID NO 140
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 140
  ccatgaaagc tccatgtcta                                     20

<210> SEQ ID NO 141
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 141
  ggcaaatgct agagacgtga                                     20

```